

SEQUENCE LISTING

<110> Klucher, Kevin M.
 Sivakumar, Pallavur V.
 Kindsvogel, Wayne R.
 Henderson, Katherine E.

<120> METHODS FOR TREATING VIRAL INFECTION
 USING IL-28 AND IL-29

<130> 02-24

<150> US 60/420,714

<151> 2002-10-23

<150> US 60/463,939

<151> 2003-04-18

<150> US 60/420,713

<151> 2002-10-23

<150> US 60/463,982

<151> 2003-04-18

<160> 40

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(618)

<221> misc_feature

<222> (0)...(0)

<223> IL-28A

<400> 1

atg	act	ggg	gac	tgc	acg	cca	gtg	ctg	gtg	ctg	atg	gcc	gca	gtg	ctg	48
Met	Thr	Gly	Asp	Cys	Thr	Pro	Val	Leu	Val	Leu	Met	Ala	Ala	Val	Leu	
1				5					10					15		

acc	gtg	act	gga	gca	gtt	cct	gtc	gcc	agg	ctc	cac	ggg	gct	ctc	ccg	96
Thr	Val	Thr	Gly	Ala	Val	Pro	Val	Ala	Arg	Leu	His	Gly	Ala	Leu	Pro	
			20					25					30			

gat	gca	agg	ggc	tgc	cac	ata	gcc	cag	ttc	aag	tcc	ctg	tct	cca	cag	144
Asp	Ala	Arg	Gly	Cys	His	Ile	Ala	Gln	Phe	Lys	Ser	Leu	Ser	Pro	Gln	
		35					40					45				

gag	ctg	cag	gcc	ttt	aag	agg	gcc	aaa	gat	gcc	tta	gaa	gag	tcg	ctt	192
Glu	Leu	Gln	Ala	Phe	Lys	Arg	Ala	Lys	Asp	Ala	Leu	Glu	Glu	Ser	Leu	
	50					55					60					

ctg	ctg	aag	gac	tgc	agg	tgc	cac	tcc	cgc	ctc	ttc	ccc	agg	acc	tgg	240
Leu	Leu	Lys	Asp	Cys	Arg	Cys	His	Ser	Arg	Leu	Phe	Pro	Arg	Thr	Trp	
65					70					75					80	
gac	ctg	agg	cag	ctg	cag	gtg	agg	gag	cgc	ccc	atg	gct	ttg	gag	gct	288
Asp	Leu	Arg	Gln	Leu	Gln	Val	Arg	Glu	Arg	Pro	Met	Ala	Leu	Glu	Ala	
			85						90					95		
gag	ctg	gcc	ctg	acg	ctg	aag	gtt	ctg	gag	gcc	acc	gct	gac	act	gac	336
Glu	Leu	Ala	Leu	Thr	Leu	Lys	Val	Leu	Glu	Ala	Thr	Ala	Asp	Thr	Asp	
			100					105					110			
cca	gcc	ctg	gtg	gac	gtc	ttg	gac	cag	ccc	ctt	cac	acc	ctg	cac	cat	384
Pro	Ala	Leu	Val	Asp	Val	Leu	Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	
		115					120					125				
atc	ctc	tcc	cag	ttc	cgg	gcc	tgt	gtg	agt	cgt	cag	ggc	ctg	ggc	acc	432
Ile	Leu	Ser	Gln	Phe	Arg	Ala	Cys	Val	Ser	Arg	Gln	Gly	Leu	Gly	Thr	
	130					135					140					
cag	atc	cag	cct	cag	ccc	acg	gca	ggg	ccc	agg	acc	cgg	ggc	cgc	ctc	480
Gln	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Thr	Arg	Gly	Arg	Leu	
145					150					155					160	
cac	cat	tgg	ctg	tac	cgg	ctc	cag	gag	gcc	cca	aaa	aag	gag	tcc	cct	528
His	His	Trp	Leu	Tyr	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Pro	
			165					170						175		
ggc	tgc	ctc	gag	gcc	tct	gtc	acc	ttc	aac	ctc	ttc	cgc	ctc	ctc	acg	576
Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr	
		180						185					190			
cga	gac	ctg	aat	tgt	gtt	gcc	agt	ggg	gac	ctg	tgt	gtc	tga			618
Arg	Asp	Leu	Asn	Cys	Val	Ala	Ser	Gly	Asp	Leu	Cys	Val	*			
		195					200					205				

<210> 2
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met Ala Ala Val Leu
 1 5 10 15
 Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala Leu Pro
 20 25 30
 Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
 35 40 45
 Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
 50 55 60
 Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp
 65 70 75 80
 Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala
 85 90 95
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp
 100 105 110
 Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
 115 120 125
 Ile Leu Ser Gln Phe Arg Ala Cys Val Ser Arg Gln Gly Leu Gly Thr

130						135						140				
Gln	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Thr	Arg	Gly	Arg	Leu	
145					150					155					160	
His	His	Trp	Leu	Tyr	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Pro	
				165					170					175		
Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr	
			180					185					190			
Arg	Asp	Leu	Asn	Cys	Val	Ala	Ser	Gly	Asp	Leu	Cys	Val				
	195						200					205				

<210> 3
 <211> 603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(603)
 <221> misc_feature
 <222> (0)...(0)
 <223> IL-29

<400> 3
 atg gct gca gct tgg acc gtg gtg ctg gtg act ttg gtg cta ggc ttg 48
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 1 5 10 15

gcc gtg gca ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag 96
 Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys
 20 25 30

ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg 144
 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
 35 40 45

agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa 192
 Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
 50 55 60

aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg 240
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
 65 70 75 80

ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc 288
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
 85 90 95

ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac 336
 Leu Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp
 100 105 110

gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc 384
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 115 120 125

cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc 432
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
 130 135 140

cgc ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag 480

Arg	Leu	His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	
145					150					155					160	
tcc	gct	ggc	tgc	ctg	gag	gca	tct	gtc	acc	ttc	aac	ctc	ttc	cgc	ctc	528
Ser	Ala	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	
				165					170					175		
ctc	acg	cga	gac	ctc	aaa	tat	gtg	gcc	gat	ggg	gac	ctg	tgt	ctg	aga	576
Leu	Thr	Arg	Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu	Cys	Leu	Arg	
			180					185					190			
acg	tca	acc	cac	cct	gag	tcc	acc	tga								603
Thr	Ser	Thr	His	Pro	Glu	Ser	Thr	*								
		195					200									

<210> 4
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 4																
Met	Ala	Ala	Ala	Trp	Thr	Val	Val	Leu	Val	Thr	Leu	Val	Leu	Gly	Leu	
1				5				10					15			
Ala	Val	Ala	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	
			20					25					30			
Gly	Cys	His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	
		35				40						45				
Ser	Phe	Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	
	50					55					60					
Asn	Trp	Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	
65					70				75					80		
Leu	Leu	Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	
			85					90					95			
Leu	Thr	Leu	Lys	Val	Leu	Glu	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp		
		100					105					110				
Val	Leu	Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	
		115					120					125				
Gln	Ala	Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	
	130					135					140					
Arg	Leu	His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	
145					150				155						160	
Ser	Ala	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	
			165						170					175		
Leu	Thr	Arg	Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu	Cys	Leu	Arg	
			180					185					190			
Thr	Ser	Thr	His	Pro	Glu	Ser	Thr									
		195					200									

<210> 5
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(615)
 <221> misc_feature
 <222> (0)...(0)
 <223> IL-28B

```

<400> 5
atg acc ggg gac tgc atg cca gtg ctg gtg ctg atg gcc gca gtg ctg 48
Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met Ala Ala Val Leu
1 5 10 15

acc gtg act gga gca gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg 96
Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro
20 25 30

gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct cca cag 144
Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
35 40 45

gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt 192
Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
50 55 60

ctg ctg aag gac tgc aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg 240
Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp
65 70 75 80

gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct 288
Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala
85 90 95

gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac act gac 336
Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp
100 105 110

cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg cac cat 384
Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
115 120 125

atc ctc tcc cag ctc cgg gcc tgt gtg agt cgt cag ggc ccg ggc acc 432
Ile Leu Ser Gln Leu Arg Ala Cys Val Ser Arg Gln Gly Pro Gly Thr
130 135 140

cag atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc cgc ctc 480
Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu
145 150 155 160

cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag tcc cct 528
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro
165 170 175

ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 576
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
180 185 190

cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 615
Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
195 200 205

```

```

<210> 6
<211> 205
<212> PRT
<213> Homo sapiens

```

```

<400> 6
Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met Ala Ala Val Leu

```

```
<210> 7
<211> 633
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (22) ... (630)
```

<400> 7																
tcacagaccc	cggagagcaa	c	atg	aag	cca	gaa	aca	gct	ggg	ggc	cac	atg				51
			Met	Lys	Pro	Glu	Thr	Ala	Gly	Gly	His	Met				
			1				5					10				
ctc	ctc	ctg	ctg	ttg	cct	ctg	ctg	ctg	gcc	gca	gtg	ctg	aca	aga	acc	99
Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Ala	Ala	Val	Leu	Thr	Arg	Thr	
				15					20					25		
caa	gct	gac	cct	gtc	ccc	agg	gcc	acc	agg	ctc	cca	gtg	gaa	gca	aag	147
Gln	Ala	Asp	Pro	Val	Pro	Arg	Ala	Thr	Arg	Leu	Pro	Val	Glu	Ala	Lys	
			30					35					40			
gat	tgc	cac	att	gct	cag	ttc	aag	tct	ctg	tcc	cca	aaa	gag	ctg	cag	195
Asp	Cys	His	Ile	Ala	Gln	Phe	Lys	Ser	Leu	Ser	Pro	Lys	Glu	Leu	Gln	
		45					50					55				
gcc	ttc	aaa	aag	gcc	aag	gat	gcc	atc	gag	aag	agg	ctg	ctt	gag	aag	243
Ala	Phe	Lys	Lys	Ala	Lys	Asp	Ala	Ile	Glu	Lys	Arg	Leu	Leu	Glu	Lys	
	60					65					70					
gac	ctg	agg	tgc	agt	tcc	cac	ctc	ttc	ccc	agg	gcc	tgg	gac	ctg	aag	291
Asp	Leu	Arg	Cys	Ser	Ser	His	Leu	Phe	Pro	Arg	Ala	Trp	Asp	Leu	Lys	
	75				80					85					90	
cag	ctg	cag	gtc	caa	gag	cgc	ccc	aag	gcc	ttg	cag	gct	gag	gtg	gcc	339

Gln	Leu	Gln	Val	Gln	Glu	Arg	Pro	Lys	Ala	Leu	Gln	Ala	Glu	Val	Ala		
				95					100					105			
ctg	acc	ctg	aag	gtc	tgg	gag	aac	atg	act	gac	tca	gcc	ctg	gcc	acc	387	
Leu	Thr	Leu	Lys	Val	Trp	Glu	Asn	Met	Thr	Asp	Ser	Ala	Leu	Ala	Thr		
			110					115					120				
atc	ctg	ggc	cag	cct	ctt	cat	aca	ctg	agc	cac	att	cac	tcc	cag	ctg	435	
Ile	Leu	Gly	Gln	Pro	Leu	His	Thr	Leu	Ser	His	Ile	His	Ser	Gln	Leu		
		125					130					135					
cag	acc	tgt	aca	cag	ctt	cag	gcc	aca	gca	gag	ccc	agg	tcc	ccg	agc	483	
Gln	Thr	Cys	Thr	Gln	Leu	Gln	Ala	Thr	Ala	Glu	Pro	Arg	Ser	Pro	Ser		
	140					145					150						
cgc	cgc	ctc	tcc	cgc	tgg	ctg	cac	agg	ctc	cag	gag	gcc	cag	agc	aag	531	
Arg	Arg	Leu	Ser	Arg	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Gln	Ser	Lys		
155					160					165					170		
gag	acc	cct	ggc	tgc	ctg	gag	gcc	tct	gtc	acc	tcc	aac	ctg	ttt	cgc	579	
Glu	Thr	Pro	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Ser	Asn	Leu	Phe	Arg		
				175					180					185			
ctg	ctc	acc	cgg	gac	ctc	aag	tgt	gtg	gcc	aat	gga	gac	cag	tgt	gtc	627	
Leu	Leu	Thr	Arg	Asp	Leu	Lys	Cys	Val	Ala	Asn	Gly	Asp	Gln	Cys	Val		
			190					195					200				
tga	cct															633	
*																	

<210> 8
 <211> 202
 <212> PRT
 <213> Mus musculus

<400> 8
 Met Lys Pro Glu Thr Ala Gly Gly His Met Leu Leu Leu Leu Leu Pro
 1 5 10 15
 Leu Leu Leu Ala Val Leu Thr Arg Thr Gln Ala Asp Pro Val Pro
 20 25 30
 Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln
 35 40 45
 Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys
 50 55 60
 Asp Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Leu Arg Cys Ser Ser
 65 70 75 80
 His Leu Phe Pro Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu
 85 90 95
 Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp
 100 105 110
 Glu Asn Met Thr Asp Ser Ala Leu Ala Thr Ile Leu Gly Gln Pro Leu
 115 120 125
 His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu
 130 135 140
 Gln Ala Thr Ala Glu Pro Arg Ser Pro Ser Arg Arg Leu Ser Arg Trp
 145 150 155 160
 Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu
 165 170 175
 Glu Ala Ser Val Thr Ser Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu
 180 185 190

Lys Cys Val Ala Asn Gly Asp Gln Cys Val
195 200

<210> 9
<211> 632
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (22)...(630)

<400> 9
tcacagaccc cggagagcaa c atg aag cca gaa aca gct ggg ggc cac atg 51
Met Lys Pro Glu Thr Ala Gly Gly His Met
1 5 10

ctc ctc ctg ctg ttg cct ctg ctg ctg gcc gca gtg ctg aca aga acc 99
Leu Leu Leu Leu Leu Pro Leu Leu Leu Ala Ala Val Leu Thr Arg Thr
15 20 25

caa gct gac cct gtc ccc agg gcc acc agg ctc cca gtg gaa gca aag 147
Gln Ala Asp Pro Val Pro Arg Ala Thr Arg Leu Pro Val Glu Ala Lys
30 35 40

gat tgc cac att gct cag ttc aag tct ctg tcc cca aaa gag ctg cag 195
Asp Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln
45 50 55

gcc ttc aaa aag gcc aag ggt gcc atc gag aag agg ctg ctt gag aag 243
Ala Phe Lys Lys Ala Lys Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys
60 65 70

gac atg agg tgc agt tcc cac ctc atc tcc agg gcc tgg gac ctg aag 291
Asp Met Arg Cys Ser Ser His Leu Ile Ser Arg Ala Trp Asp Leu Lys
75 80 85 90

cag ctg cag gtc caa gag cgc ccc aag gcc ttg cag gct gag gtg gcc 339
Gln Leu Gln Val Gln Glu Arg Pro Lys Ala Leu Gln Ala Glu Val Ala
95 100 105

ctg acc ctg aag gtc tgg gag aac ata aat gac tca gcc ctg acc acc 387
Leu Thr Leu Lys Val Trp Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr
110 115 120

atc ctg ggc cag cct ctt cat aca ctg agc cac att cac tcc cag ctg 435
Ile Leu Gly Gln Pro Leu His Thr Leu Ser His Ile His Ser Gln Leu
125 130 135

cag acc tgt aca cag ctt cag gcc aca gca gag ccc aag ccc ccg agt 483
Gln Thr Cys Thr Gln Leu Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser
140 145 150

cgc cgc ctc tcc cgc tgg ctg cac agg ctc cag gag gcc cag agc aag 531
Arg Arg Leu Ser Arg Trp Leu His Arg Leu Gln Glu Ala Gln Ser Lys
155 160 165 170

gag act cct ggc tgc ctg gag gac tct gtc acc tcc aac ctg ttt caa 579
Glu Thr Pro Gly Cys Leu Glu Asp Ser Val Thr Ser Asn Leu Phe Gln
175 180 185


```

ctg ctc ctc cgg gac ctc aag tgt gtg gcc agt gga gac cag tgt gtc 627
Leu Leu Leu Arg Asp Leu Lys Cys Val Ala Ser Gly Asp Gln Cys Val
      190                      195                200

```

```

tga cc 632
*
```

```

<210> 10
<211> 202
<212> PRT
<213> Mus musculus

```

```

<400> 10
Met Lys Pro Glu Thr Ala Gly Gly His Met Leu Leu Leu Leu Leu Pro
 1      5      10      15
Leu Leu Leu Ala Val Leu Thr Arg Thr Gln Ala Asp Pro Val Pro
      20      25      30
Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln
      35      40      45
Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys
      50      55      60
Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Met Arg Cys Ser Ser
      65      70      75      80
His Leu Ile Ser Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu
      85      90      95
Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp
      100     105     110
Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr Ile Leu Gly Gln Pro Leu
      115     120     125
His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu
      130     135     140
Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser Arg Arg Leu Ser Arg Trp
      145     150     155     160
Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu
      165     170     175
Glu Asp Ser Val Thr Ser Asn Leu Phe Gln Leu Leu Leu Arg Asp Leu
      180     185     190
Lys Cys Val Ala Ser Gly Asp Gln Cys Val
      195                200

```

```

<210> 11
<211> 1563
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)...(1563)

<221> misc_feature
<222> (0)...(0)
<223> IL-28RA

```

```

<400> 11
atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag 48
Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1      5      10      15

gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96

```

Ala	Ala	Pro	Gly	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu	
			20					25					30			
ctc	tcc	cag	aac	ttc	agc	gtg	tac	ctg	aca	tgg	ctc	cca	ggg	ctt	ggc	144
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly	
		35					40					45				
aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc	192
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	
	50					55					60					
cgt	aga	cgg	tgg	cgc	gaa	gtg	gaa	gag	tgt	gcg	gga	acc	aag	gag	ctg	240
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu	
65					70					75					80	
cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc	288
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe	
				85					90					95		
aag	gga	cgc	gtg	cgg	acg	gtt	tct	ccc	agc	tcc	aag	tcc	ccc	tgg	gtg	336
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val	
			100					105					110			
gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct	384
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro	
		115					120					125				
gtc	ctg	gtg	ctc	acc	cag	acg	gag	gag	atc	ctg	agt	gcc	aat	gcc	acg	432
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr	
	130					135					140					
tac	cag	ctg	ccc	ccc	tgc	atg	ccc	cca	ctg	gat	ctg	aag	tat	gag	gtg	480
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val	
145					150					155					160	
gca	ttc	tgg	aag	gag	ggg	gcc	gga	aac	aag	acc	cta	ttt	cca	gtc	act	528
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr	
				165					170					175		
ccc	cat	ggc	cag	cca	gtc	cag	atc	act	ctc	cag	cca	gct	gcc	agc	gaa	576
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu	
			180					185					190			
cac	cac	tgc	ctc	agt	gcc	aga	acc	atc	tac	acg	ttc	agt	gtc	ccg	aaa	624
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys	
		195					200					205				
tac	agc	aag	ttc	tct	aag	ccc	acc	tgc	ttc	ttg	ctg	gag	gtc	cca	gaa	672
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu	
	210					215					220					
gcc	aac	tgg	gct	ttc	ctg	gtg	ctg	cca	tcg	ctt	ctg	ata	ctg	ctg	tta	720
Ala	Asn	Trp	Ala	Phe	Leu	Val	Leu	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	
225					230					235					240	
gta	att	gcc	gca	ggg	ggg	gtg	atc	tgg	aag	acc	ctc	atg	ggg	aac	ccc	768
Val	Ile	Ala	Ala	Gly	Gly	Val	Ile	Trp	Lys	Thr	Leu	Met	Gly	Asn	Pro	
				245					250					255		
tgg	ttt	cag	cgg	gca	aag	atg	cca	cgg	gcc	ctg	gac	ttt	tct	gga	cac	816
Trp	Phe	Gln	Arg	Ala	Lys	Met	Pro	Arg	Ala	Leu	Asp	Phe	Ser	Gly	His	
			260					265					270			

aca	cac	cct	gtg	gca	acc	ttt	cag	ccc	agc	aga	cca	gag	tcc	gtg	aat	864
Thr	His	Pro	Val	Ala	Thr	Phe	Gln	Pro	Ser	Arg	Pro	Glu	Ser	Val	Asn	
		275					280					285				
gac	ttg	ttc	ctc	tgt	ccc	caa	aag	gaa	ctg	acc	aga	ggg	gtc	agg	ccg	912
Asp	Leu	Phe	Leu	Cys	Pro	Gln	Lys	Glu	Leu	Thr	Arg	Gly	Val	Arg	Pro	
	290					295					300					
acg	cct	cga	gtc	agg	gcc	cca	gcc	acc	caa	cag	aca	aga	tgg	aag	aag	960
Thr	Pro	Arg	Val	Arg	Ala	Pro	Ala	Thr	Gln	Gln	Thr	Arg	Trp	Lys	Lys	
305					310					315					320	
gac	ctt	gca	gag	gac	gaa	gag	gag	gag	gat	gag	gag	gac	aca	gaa	gat	1008
Asp	Leu	Ala	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Asp	Thr	Glu	Asp	
				325					330					335		
ggc	gtc	agc	ttc	cag	ccc	tac	att	gaa	cca	cct	tct	ttc	ctg	ggg	caa	1056
Gly	Val	Ser	Phe	Gln	Pro	Tyr	Ile	Glu	Pro	Pro	Ser	Phe	Leu	Gly	Gln	
			340					345					350			
gag	cac	cag	gct	cca	ggg	cac	tcg	gag	gct	ggg	ggg	gtg	gac	tca	ggg	1104
Glu	His	Gln	Ala	Pro	Gly	His	Ser	Glu	Ala	Gly	Gly	Val	Asp	Ser	Gly	
		355					360					365				
agg	ccc	agg	gct	cct	ctg	gtc	cca	agc	gaa	ggc	tcc	tct	gct	tgg	gat	1152
Arg	Pro	Arg	Ala	Pro	Leu	Val	Pro	Ser	Glu	Gly	Ser	Ser	Ala	Trp	Asp	
	370					375					380					
tct	tca	gac	aga	agc	tgg	gcc	agc	act	gtg	gac	tcc	tcc	tgg	gac	agg	1200
Ser	Ser	Asp	Arg	Ser	Trp	Ala	Ser	Thr	Val	Asp	Ser	Ser	Trp	Asp	Arg	
385					390					395					400	
gct	ggg	tcc	tct	ggc	tat	ttg	gct	gag	aag	ggg	cca	ggc	caa	ggg	ccg	1248
Ala	Gly	Ser	Ser	Gly	Tyr	Leu	Ala	Glu	Lys	Gly	Pro	Gly	Gln	Gly	Pro	
				405				410						415		
ggg	ggg	gat	ggg	cac	caa	gaa	tct	ctc	cca	cca	cct	gaa	ttc	tcc	aag	1296
Gly	Gly	Asp	Gly	His	Gln	Glu	Ser	Leu	Pro	Pro	Pro	Glu	Phe	Ser	Lys	
			420					425					430			
gac	tcg	ggg	ttc	ctg	gaa	gag	ctc	cca	gaa	gat	aac	ctc	tcc	tcc	tgg	1344
Asp	Ser	Gly	Phe	Leu	Glu	Glu	Leu	Pro	Glu	Asp	Asn	Leu	Ser	Ser	Trp	
		435					440					445				
gcc	acc	tgg	ggc	acc	tta	cca	ccg	gag	ccg	aat	ctg	gtc	cct	ggg	gga	1392
Ala	Thr	Trp	Gly	Thr	Leu	Pro	Pro	Glu	Pro	Asn	Leu	Val	Pro	Gly	Gly	
	450					455					460					
ccc	cca	gtt	tct	ctt	cag	aca	ctg	acc	ttc	tgc	tgg	gaa	agc	agc	cct	1440
Pro	Pro	Val	Ser	Leu	Gln	Thr	Leu	Thr	Phe	Cys	Trp	Glu	Ser	Ser	Pro	
465					470					475					480	
gag	gag	gaa	gag	gag	gag	gag	gag	gag	tca	gaa	att	gag	gac	agc	gat	1488
Glu	Glu	Glu	Glu	Glu	Glu	Ala	Arg	Glu	Ser	Glu	Ile	Glu	Asp	Ser	Asp	
				485						490					495	
ggc	agc	tgg	ggg	gct	gag	agc	acc	cag	agg	acc	gag	gac	agg	ggc	cgg	1536
Gly	Ser	Trp	Gly	Ala	Glu	Ser	Thr	Gln	Arg	Thr	Glu	Asp	Arg	Gly	Arg	
			500					505					510			
aca	ttg	ggg	cat	tac	atg	gcc	agg	tga								1563

Thr Leu Gly His Tyr Met Ala Arg *
 515 520

<210> 12
 <211> 520
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
 165 170 175
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu
 225 230 235 240
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His
 260 265 270
 Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn
 275 280 285
 Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro
 290 295 300
 Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys
 305 310 315 320
 Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp
 325 330 335
 Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln
 340 345 350
 Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly
 355 360 365
 Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp
 370 375 380
 Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg
 385 390 395 400
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415

Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
 420 425 430
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
 435 440 445
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
 485 490 495
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
 500 505 510
 Thr Leu Gly His Tyr Met Ala Arg
 515 520

<210> 13
 <211> 1476
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1476)
 <221> misc_feature
 <222> (0)...(0)
 <223> IL-28RA splice variant

<400> 13
 atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag 48
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15

 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30

 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45

 aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60

 cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80

 cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95

 aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110

 gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct 384
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125

gtc	ctg	gtg	ctc	acc	cag	acg	gag	gag	atc	ctg	agt	gcc	aat	gcc	acg	432
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr	
	130					135					140					
tac	cag	ctg	ccc	ccc	tgc	atg	ccc	cca	ctg	ttt	ctg	aag	tat	gag	gtg	480
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Phe	Leu	Lys	Tyr	Glu	Val	
145					150					155					160	
gca	ttt	tgg	ggg	ggg	ggg	gcc	gga	acc	aag	acc	cta	ttt	cca	gtc	act	528
Ala	Phe	Trp	Gly	Gly	Gly	Ala	Gly	Thr	Lys	Thr	Leu	Phe	Pro	Val	Thr	
				165					170					175		
ccc	cat	ggc	cag	cca	gtc	cag	atc	act	ctc	cag	cca	gct	gcc	agc	gaa	576
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu	
			180					185					190			
cac	cac	tgc	ctc	agt	gcc	aga	acc	atc	tac	acg	ttc	agt	gtc	ccg	aaa	624
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys	
		195					200					205				
tac	agc	aag	ttc	tct	aag	ccc	acc	tgc	ttc	ttg	ctg	gag	gtc	cca	gaa	672
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu	
	210					215					220					
gcc	aac	tgg	gct	ttc	ctg	gtg	ctg	cca	tgc	ctt	ctg	ata	ctg	ctg	tta	720
Ala	Asn	Trp	Ala	Phe	Leu	Val	Leu	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	
225					230					235					240	
gta	att	gcc	gca	ggg	ggt	gtg	atc	tgg	aag	acc	ctc	atg	ggg	aac	ccc	768
Val	Ile	Ala	Ala	Gly	Gly	Val	Ile	Trp	Lys	Thr	Leu	Met	Gly	Asn	Pro	
				245					250					255		
tgg	ttt	cag	cgg	gca	aag	atg	cca	cgg	gcc	ctg	gaa	ctg	acc	aga	ggg	816
Trp	Phe	Gln	Arg	Ala	Lys	Met	Pro	Arg	Ala	Leu	Glu	Leu	Thr	Arg	Gly	
			260					265					270			
gtc	agg	ccg	acg	cct	cga	gtc	agg	gcc	cca	gcc	acc	caa	cag	aca	aga	864
Val	Arg	Pro	Thr	Pro	Arg	Val	Arg	Ala	Pro	Ala	Thr	Gln	Gln	Thr	Arg	
		275					280					285				
tgg	aag	aag	gac	ctt	gca	gag	gac	gaa	gag	gag	gag	gat	gag	gag	gac	912
Trp	Lys	Lys	Asp	Leu	Ala	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Asp	
	290					295					300					
aca	gaa	gat	ggc	gtc	agc	ttc	cag	ccc	tac	att	gaa	cca	cct	tct	ttc	960
Thr	Glu	Asp	Gly	Val	Ser	Phe	Gln	Pro	Tyr	Ile	Glu	Pro	Pro	Ser	Phe	
305					310					315					320	
ctg	ggg	caa	gag	cac	cag	gct	cca	ggg	cac	tcg	gag	gct	ggt	ggg	gtg	1008
Leu	Gly	Gln	Glu	His	Gln	Ala	Pro	Gly	His	Ser	Glu	Ala	Gly	Gly	Val	
				325					330					335		
gac	tca	ggg	agg	ccc	agg	gct	cct	ctg	gtc	cca	agc	gaa	ggc	tcc	tct	1056
Asp	Ser	Gly	Arg	Pro	Arg	Ala	Pro	Leu	Val	Pro	Ser	Glu	Gly	Ser	Ser	
			340					345					350			
gct	tgg	gat	tct	tca	gac	aga	agc	tgg	gcc	agc	act	gtg	gac	tcc	tcc	1104
Ala	Trp	Asp	Ser	Ser	Asp	Arg	Ser	Trp	Ala	Ser	Thr	Val	Asp	Ser	Ser	
		355					360					365				
tgg	gac	agg	gct	ggg	tcc	tct	ggc	tat	ttg	gct	gag	aag	ggg	cca	ggc	1152
Trp	Asp	Arg	Ala	Gly	Ser	Ser	Gly	Tyr	Leu	Ala	Glu	Lys	Gly	Pro	Gly	

370	375	380	
caa ggg ccg ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa			1200
Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu			
385	390	395	400
ttc tcc aag gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc			1248
Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu			
	405	410	415
tcc tcc tgg gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc			1296
Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val			
	420	425	430
cct ggg gga ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa			1344
Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu			
	435	440	445
agc agc cct gag gag gaa gag gag gcg agg gaa tca gaa att gag gac			1392
Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp			
	450	455	460
agc gat gcg ggc agc tgg ggg gct gag agc acc cag agg acc gag gac			1440
Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp			
	465	470	475
agg ggc cgg aca ttg ggg cat tac atg gcc agg tga			1476
Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg *			
	485	490	

<210> 14
 <211> 491
 <212> PRT
 <213> Homo sapiens

<400> 14

Met	Ala	Gly	Pro	Glu	Arg	Trp	Gly	Pro	Leu	Leu	Leu	Cys	Leu	Leu	Gln
1				5					10					15	
Ala	Ala	Pro	Gly	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu
			20					25					30		
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly
		35					40					45			
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr
	50					55					60				
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu
65					70				75					80	
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe
			85						90					95	
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
			100					105					110		
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
		115					120					125			
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr
	130					135					140				
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Phe	Leu	Lys	Tyr	Glu	Val
145					150					155				160	
Ala	Phe	Trp	Gly	Gly	Gly	Ala	Gly	Thr	Lys	Thr	Leu	Phe	Pro	Val	Thr
			165					170						175	
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu
			180					185					190		
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys

```

<210> 15
<211> 674
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(636)

<221> misc_feature
<222> (0)...(0)
<223> IL-28RA soluble variant

<400> 15
atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag      48
Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
  1                      5                      10                      15

gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg      96
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
                      20                      25                      30

ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc      144

```


Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly		
		35					40					45					
aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc	192	
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr		
	50					55					60						
cgt	aga	cgg	tgg	cgc	gaa	gtg	gaa	gag	tgt	gcg	gga	acc	aag	gag	ctg	240	
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu		
	65				70					75					80		
cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc	288	
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe		
				85					90					95			
aag	gga	cgc	gtg	cgg	acg	gtt	tct	ccc	agc	tcc	aag	tcc	ccc	tgg	gtg	336	
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val		
			100					105					110				
gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct	384	
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro		
		115					120						125				
gtc	ctg	gtg	ctc	acc	cag	acg	gag	gag	atc	ctg	agt	gcc	aat	gcc	acg	432	
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr		
	130					135					140						
tac	cag	ctg	ccc	ccc	tgc	atg	ccc	cca	ctg	gat	ctg	aag	tat	gag	gtg	480	
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val		
	145				150					155					160		
gca	ttc	tgg	aag	gag	ggg	gcc	gga	aac	aag	gtg	gga	agc	tcc	ttt	cct	528	
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Val	Gly	Ser	Ser	Phe	Pro		
				165				170						175			
gcc	ccc	agg	cta	ggc	ccg	ctc	ctc	cac	ccc	ttc	tta	ctc	agg	ttc	ttc	576	
Ala	Pro	Arg	Leu	Gly	Pro	Leu	Leu	His	Pro	Phe	Leu	Leu	Arg	Phe	Phe		
			180					185					190				
tca	ccc	tcc	cag	cct	gct	cct	gca	ccc	ctc	ctc	cag	gaa	gtc	ttc	cct	624	
Ser	Pro	Ser	Gln	Pro	Ala	Pro	Ala	Pro	Leu	Leu	Gln	Glu	Val	Phe	Pro		
		195					200					205					
gta	cac	tcc	tga	cttctggcag	tcagccctaa	taaaatctga	tcaaagta									674	
Val	His	Ser	*														
	210																

<210> 16

<211> 211

<212> PRT

<213> Homo sapiens

<400> 16

Met	Ala	Gly	Pro	Glu	Arg	Trp	Gly	Pro	Leu	Leu	Leu	Cys	Leu	Leu	Gln		
1				5				10					15				
Ala	Ala	Pro	Gly	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu		
		20						25				30					
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly		
	35						40					45					
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr		
	50					55					60						

Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu
65					70					75					80
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe
			85						90					95	
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
			100					105					110		
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
		115					120					125			
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr
	130				135						140				
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val
145					150					155					160
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Val	Gly	Ser	Ser	Phe	Pro
			165					170						175	
Ala	Pro	Arg	Leu	Gly	Pro	Leu	Leu	His	Pro	Phe	Leu	Leu	Arg	Phe	Phe
			180					185					190		
Ser	Pro	Ser	Gln	Pro	Ala	Pro	Ala	Pro	Leu	Leu	Gln	Glu	Val	Phe	Pro
		195					200					205			
Val	His	Ser													
	210														

<210> 17
 <211> 734
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> (53)...(127)
 <221> mat_peptide
 <222> (128)...(655)

<221> CDS
 <222> (53)...(655)

<400> 17
 tgggtgacag cctcagagtg tttcttctgc tgacaaagac cagagatcag ga atg aaa 58
 Met Lys
 -25

cta	gac	atg	act	ggg	gac	tgc	acg	cca	gtg	ctg	gtg	ctg	atg	gcc	gca	106
Leu	Asp	Met	Thr	Gly	Asp	Cys	Thr	Pro	Val	Leu	Val	Leu	Met	Ala	Ala	
			-20					-15					-10			

gtg	ctg	acc	gtg	act	gga	gca	gtt	cct	gtc	gcc	agg	ctc	cac	ggg	gct	154
Val	Leu	Thr	Val	Thr	Gly	Ala	Val	Pro	Val	Ala	Arg	Leu	His	Gly	Ala	
		-5					1				5					

ctc	ccg	gat	gca	agg	ggc	tgc	cac	ata	gcc	cag	ttc	aag	tcc	ctg	tct	202
Leu	Pro	Asp	Ala	Arg	Gly	Cys	His	Ile	Ala	Gln	Phe	Lys	Ser	Leu	Ser	
10					15					20					25	

cca	cag	gag	ctg	cag	gcc	ttt	aag	agg	gcc	aaa	gat	gcc	tta	gaa	gag	250
Pro	Gln	Glu	Leu	Gln	Ala	Phe	Lys	Arg	Ala	Lys	Asp	Ala	Leu	Glu	Glu	
				30					35					40		

tcg	ctt	ctg	ctg	aag	gac	tgc	agg	tgc	cac	tcc	cgc	ctc	ttc	ccc	agg	298
Ser	Leu	Leu	Leu	Lys	Asp	Cys	Arg	Cys	His	Ser	Arg	Leu	Phe	Pro	Arg	
			45					50					55			

```

acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg 346
Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu
      60                      65                      70

gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac 394
Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp
      75                      80                      85

act gac cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg 442
Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu
      90                      95                      100

cac cat atc ctc tcc cag ttc cgg gcc tgt atc cag cct cag ccc acg 490
His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr
      110                      115                      120

gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg tac cgg ctc 538
Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu Tyr Arg Leu
      125                      130                      135

cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc 586
Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val
      140                      145                      150

acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctg aat tgt gtt gcc 634
Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala
      155                      160                      165

agt ggg gac ctg tgt gtc tga ccctcccacc agtcatgcaa cctgagattt 685
Ser Gly Asp Leu Cys Val *
      170                      175

tatttataaaa ttagccactt gtcttaattt attgccaccc agtcgctat 734

```

```

<210> 18
<211> 200
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> (1)...(25)

```

```

<400> 18
Met Lys Leu Asp Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met
-25 -20 -15 -10
Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His
      -5                      1                      5
Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser
      10                      15                      20
Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu
      25                      30                      35
Glu Glu Ser Leu Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe
40 45 50 55
Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met
      60                      65                      70
Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr
      75                      80                      85
Ala Asp Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His
      90                      95                      100
Thr Leu His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln
105 110 115

```

```

Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu Tyr
120                               125           130           135
Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala
                               140           145           150
Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys
                               155           160           165
Val Ala Ser Gly Asp Leu Cys Val
                               170           175

```

```

<210> 19
<211> 856
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> sig_peptide
<222> (98)...(154)

<221> mat_peptide
<222> (155)...(700)

```

```

<221> CDS
<222> (98)...(700)

```

```

<400> 19
aattaccttt tcaactttaca cacatcatct tggattgccc atttttgcgtg gctaaaaagc 60
agagccatgc cgctgggggaa gcagttgcga ttttagcc atg gct gca gct tgg acc 115
                               Met Ala Ala Ala Trp Thr
                               -15

```

```

gtg gtg ctg gtg act ttg gtg cta ggc ttg gcc gtg gca ggc cct gtc 163
Val Val Leu Val Thr Leu Val Leu Gly Leu Ala Val Ala Gly Pro Val
                               -10           -5           1

```

```

ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg 211
Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg
                               5           10           15

```

```

ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg 259
Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
20           25           30           35

```

```

gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct 307
Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
                               40           45           50

```

```

cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag 355
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu
55           60           65

```

```

cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg 403
Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
70           75           80

```

```

gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt 451
Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
85           90           95

```

```

cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct 499
His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
100           105           110           115

```

```

cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg 547
Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu
120 125 130

cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag 595
His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu
135 140 145

gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa 643
Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
150 155 160

tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca acc cac cct gag 691
Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr His Pro Glu
165 170 175

tcc acc tga caccacac cttatttatg cgctgagccc tactccttcc 740
Ser Thr *
180

ttaatttatt tcctctcacc ctttatttat gaagctgcag ccctgactga gacatagggc 800
tgagtttatt gttttacttt tatacattat gcacaaataa acaacaagga attgga 856

<210> 20
<211> 200
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 20
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
-15 -10 -5
Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys
1 5 10
Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
15 20 25
Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
30 35 40 45
Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
50 55 60
Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
65 70 75
Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp
80 85 90
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
95 100 105
Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
110 115 120 125
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
130 135 140
Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145 150 155
Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg
160 165 170
Thr Ser Thr His Pro Glu Ser Thr
175 180

```

<210> 21
 <211> 734
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> (53)...(127)

<221> mat_peptide
 <222> (128)...(655)

<221> CDS
 <222> (53)...(655)

<400> 21
 tgggtgacag cctcagagtg tttcttctgc tgacaaagac cagagatcag ga atg aaa 58
 Met Lys
 -25

cta gac atg acc ggg gac tgc atg cca gtg ctg gtg ctg atg gcc gca 106
 Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met Ala Ala
 -20 -15 -10

gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cgc ggg gct 154
 Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala
 -5 1 5

ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct 202
 Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser
 10 15 20 25

cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag 250
 Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu
 30 35 40

tcg ctt ctg ctg aag gac tgc aag tgc cgc tcc cgc ctc ttc ccc agg 298
 Ser Leu Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg
 45 50 55

acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg 346
 Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu
 60 65 70

gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac 394
 Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp
 75 80 85

act gac cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg 442
 Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu
 90 95 100 105

cac cat atc ctc tcc cag ctc cgg gcc tgt atc cag cct cag ccc acg 490
 His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr
 110 115 120

gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg cac cgg ctc 538
 Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His Arg Leu
 125 130 135

cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc 586
 Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val

```

140              145              150
acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctg aat tgt gtt gcc 634
Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala
155              160              165

agc ggg gac ctg tgt gtc tga cccttccgcc agtcatgcaa cctgagattt 685
Ser Gly Asp Leu Cys Val *
170              175

tatttataaaa ttagccactt ggcttaattt attgccaccc agtcgctat 734

```

```

<210> 22
<211> 200
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> (1)...(25)

```

```

<400> 22
Met Lys Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met
-25              -20              -15              -10
Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg
-5              1              5
Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser
10              15              20
Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu
25              30              35
Glu Glu Ser Leu Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe
40              45              50              55
Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val
60              65              70
Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr
75              80              85
Ala Asp Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His
90              95              100
Thr Leu His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln
105              110              115
Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His
120              125              130              135
Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala
140              145              150
Ser Val Thr Phe Asn Leu Phe Arg Leu Thr Arg Asp Leu Asn Cys
155              160              165
Val Ala Ser Gly Asp Leu Cys Val
170              175

```

```

<210> 23
<211> 528
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> IL-28A mutant C48S

```

```

<221> CDS
<222> (1)...(528)

```

```

<400> 23

```

```

gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc tgc 48
Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
1 5 10 15

cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20 25 30

aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tcc 144
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Ser
35 40 45

agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
50 55 60

cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac 288
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
85 90 95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc 336
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
100 105 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
115 120 125

cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag 432
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
130 135 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145 150 155 160

ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga 528
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *
165 170 175

```

```

<210> 24
<211> 175
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> IL-28A mutant C48S

```

```

<400> 24
Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
1 5 10 15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20 25 30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Ser
35 40 45
Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu

```


50		55		60
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr				
65		70		75
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp				
	85		90	95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe				
	100		105	110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly				
	115		120	125
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu				
	130		135	140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu				
145		150	155	160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val				
	165		170	175

<210> 25
 <211> 531
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> met IL-28A mutant C49S

<221> CDS
 <222> (1)...(531)

<400> 25	
atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc	48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly	
1 5 10 15	
tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc	96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala	
20 25 30	
ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac	144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp	
35 40 45	
tcc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag	192
Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln	
50 55 60	
ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg	240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu	
65 70 75 80	
acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg	288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val	
85 90 95	
gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag	336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln	
100 105 110	
ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg	384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg	
115 120 125	
ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag	432

Gly	Arg	Leu	His	His	Trp	Leu	Tyr	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	
130						135					140					
gag	tcc	cct	ggc	tgc	ctc	gag	gcc	tct	gtc	acc	ttc	aac	ctc	ttc	cgc	480
Glu	Ser	Pro	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	
145					150					155					160	
ctc	ctc	acg	cga	gac	ctg	aat	tgt	gtt	gcc	agt	ggg	gac	ctg	tgt	gtc	528
Leu	Leu	Thr	Arg	Asp	Leu	Asn	Cys	Val	Ala	Ser	Gly	Asp	Leu	Cys	Val	
				165					170						175	
tga																531
*																

<210> 26
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> met IL-28A mutant C49S

Met	Val	Pro	Val	Ala	Arg	Leu	His	Gly	Ala	Leu	Pro	Asp	Ala	Arg	Gly	
1				5				10						15		
Cys	His	Ile	Ala	Gln	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Gln	Ala	
		20						25					30			
Phe	Lys	Arg	Ala	Lys	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Leu	Leu	Lys	Asp	
	35					40						45				
Ser	Arg	Cys	His	Ser	Arg	Leu	Phe	Pro	Arg	Thr	Trp	Asp	Leu	Arg	Gln	
	50					55					60					
Leu	Gln	Val	Arg	Glu	Arg	Pro	Met	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	
65					70					75					80	
Thr	Leu	Lys	Val	Leu	Glu	Ala	Thr	Ala	Asp	Thr	Asp	Pro	Ala	Leu	Val	
			85						90					95		
Asp	Val	Leu	Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	
		100						105					110			
Phe	Arg	Ala	Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Thr	Arg	
	115						120					125				
Gly	Arg	Leu	His	His	Trp	Leu	Tyr	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	
	130					135					140					
Glu	Ser	Pro	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	
145					150					155					160	
Leu	Leu	Thr	Arg	Asp	Leu	Asn	Cys	Val	Ala	Ser	Gly	Asp	Leu	Cys	Val	
				165					170						175	

<210> 27
 <211> 528
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-28A mutant C50S

<221> CDS
 <222> (1)...(528)

ggt	cct	gtc	gcc	agg	ctc	cac	ggg	gct	ctc	ccg	gat	gca	agg	ggc	tgc	48
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Val	Pro	Val	Ala	Arg	Leu	His	Gly	Ala	Leu	Pro	Asp	Ala	Arg	Gly	Cys	
1				5					10					15		
cac	ata	gcc	cag	ttc	aag	tcc	ctg	tct	cca	cag	gag	ctg	cag	gcc	ttt	96
His	Ile	Ala	Gln	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Gln	Ala	Phe	
			20					25					30			
aag	agg	gcc	aaa	gat	gcc	tta	gaa	gag	tcg	ctt	ctg	ctg	aag	gac	tgc	144
Lys	Arg	Ala	Lys	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Leu	Leu	Lys	Asp	Cys	
		35					40					45				
agg	tcc	cac	tcc	cgc	ctc	ttc	ccc	agg	acc	tgg	gac	ctg	agg	cag	ctg	192
Arg	Ser	His	Ser	Arg	Leu	Phe	Pro	Arg	Thr	Trp	Asp	Leu	Arg	Gln	Leu	
	50					55					60					
cag	gtg	agg	gag	cgc	ccc	atg	gct	ttg	gag	gct	gag	ctg	gcc	ctg	acg	240
Gln	Val	Arg	Glu	Arg	Pro	Met	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	
65					70				75						80	
ctg	aag	gtt	ctg	gag	gcc	acc	gct	gac	act	gac	cca	gcc	ctg	gtg	gac	288
Leu	Lys	Val	Leu	Glu	Ala	Thr	Ala	Asp	Thr	Asp	Pro	Ala	Leu	Val	Asp	
			85					90						95		
gtc	ttg	gac	cag	ccc	ctt	cac	acc	ctg	cac	cat	atc	ctc	tcc	cag	ttc	336
Val	Leu	Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Phe	
			100					105					110			
cgg	gcc	tgt	atc	cag	cct	cag	ccc	acg	gca	ggg	ccc	agg	acc	cgg	ggc	384
Arg	Ala	Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Thr	Arg	Gly	
		115					120					125				
cgc	ctc	cac	cat	tgg	ctg	tac	cgg	ctc	cag	gag	gcc	cca	aaa	aag	gag	432
Arg	Leu	His	His	Trp	Leu	Tyr	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	
	130					135					140					
tcc	cct	ggc	tgc	ctc	gag	gcc	tct	gtc	acc	ttc	aac	ctc	ttc	cgc	ctc	480
Ser	Pro	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	
145					150					155					160	
ctc	acg	cga	gac	ctg	aat	tgt	gtt	gcc	agt	ggg	gac	ctg	tgt	gtc	tga	528
Leu	Thr	Arg	Asp	Leu	Asn	Cys	Val	Ala	Ser	Gly	Asp	Leu	Cys	Val	*	
				165					170					175		

<210> 28
 <211> 175
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-28A mutant C50S

Val	Pro	Val	Ala	Arg	Leu	His	Gly	Ala	Leu	Pro	Asp	Ala	Arg	Gly	Cys	
1				5					10					15		
His	Ile	Ala	Gln	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Gln	Ala	Phe	
			20					25					30			
Lys	Arg	Ala	Lys	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Leu	Leu	Lys	Asp	Cys	
		35					40					45				

```

Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50          55          60
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65          70          75          80
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
          85          90          95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
          100          105          110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
          115          120          125
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
          130          135          140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
          145          150          155          160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
          165          170          175

```

```

<210> 29
<211> 531
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> met IL-28A mutant C51S

```

```

<221> CDS
<222> (1)...(531)

```

```

<400> 29
atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc      48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1          5          10          15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc      96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
          20          25          30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac      144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
          35          40          45

tgc agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag      192
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
          50          55          60

ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg      240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
          65          70          75          80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg      288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
          85          90          95

gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag      336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
          100          105          110

ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg      384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
          115          120          125

```

```

ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag 432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
      130              135              140

```

```

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145              150              155              160

```

```

ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc 528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
              165              170              175

```

```

tga 531
*
```

```

<210> 30
<211> 176
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> met IL-28A mutant C51S

```

```

<400> 30
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1      5      10      15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20      25      30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35      40      45
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50      55      60
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65      70      75      80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85      90      95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100     105     110
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115     120     125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130     135     140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145     150     155     160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165     170     175

```

```

<210> 31
<211> 546
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> IL-29 mutant C171S

```

```

<221> CDS
<222> (1)...(546)

```

```

<400> 31

```

```

ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc cac 48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
1 5 10 15

atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc aaa 96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
20 25 30

aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct 144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
35 40 45

tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag 192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
50 55 60

gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc ctg 240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65 70 75 80

aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg gat 288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
85 90 95

cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct tgc 336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
100 105 110

att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac 384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
115 120 125

cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct ggt 432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
130 135 140

tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt 480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145 150 155 160

gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct acc 528
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser Thr
165 170 175

cat ccg gaa tct acc taa
His Pro Glu Ser Thr * 546
180

```

```

<210> 32
<211> 181
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> IL-29 mutant C171S

```

```

<400> 32
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
1 5 10 15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
20 25 30

```

[illegible]

```
<210> 33
<211> 549
<212> DNA
<213> Artificial Sequence
```

<220>
<223> met IL-29 mutant C172S

```
<221> CDS
<222> (1) . . . (549)
```

<400> 33																
atg	ggg	ccg	gtt	ccg	acc	tct	aaa	cca	acc	acc	act	ggg	aaa	ggg	tgc	48
Met	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys	
1				5					10					15		
cac	atc	ggg	cgt	ttc	aaa	tct	ctg	tct	ccg	cag	gaa	ctg	gct	tct	ttc	96
His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	
			20					25					30			
aaa	aaa	gct	cgt	gac	gct	ctg	gaa	gaa	tct	ctg	aaa	ctg	aaa	aac	tgg	144
Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	
		35					40					45				
tct	tgc	tct	tct	ccg	gtt	ttc	ccg	ggg	aac	tgg	gat	ctg	cgt	ctg	ctg	192
Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	
	50					55					60					
cag	gtt	cgt	gaa	cgt	ccg	gtt	gct	ctg	gaa	gct	gaa	ctg	gct	ctg	acc	240
Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	
65					70				75						80	
ctg	aaa	gtt	ctg	gaa	gct	gct	gca	ggg	cct	gct	ctg	gaa	gat	gtt	ctg	288
Leu	Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	
				85					90					95		
gat	cag	ccg	ctg	cac	act	ctg	cac	cac	atc	ctg	tct	cag	ctg	cag	gct	336
Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala	
			100				105						110			

```

tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg 384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
      115                120                125

cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
      130                135                140

ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                150                155                160

cgt gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct 528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser
      165                170                175

acc cat ccg gaa tct acc taa
Thr His Pro Glu Ser Thr * 549
      180

```

```

<210> 34
<211> 182
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> met IL-29 mutant C172S

```

```

<400> 34
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1      5      10      15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
      20      25      30
Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
      35      40      45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
      50      55      60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
      65      70      75      80
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
      85      90      95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
      100      105      110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
      115      120      125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
      130      135      140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                150                155                160

```


Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 35
 <211> 531
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> met IL-28A

<221> CDS
 <222> (1)...(531)

<400> 35
 atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc 48
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40 45
 tgc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
 Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95
 gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag 432
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

tga
*

531

<210> 36
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-28A

<400> 36
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35 40 45
Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
85 90 95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

<210> 37
<211> 621
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-29

<221> CDS
<222> (1)...(549)

<400> 37
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
1 5 10 15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45

```

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
      50                55                60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
      65                70                75                80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                90                95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
                100                105                110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
                115                120                125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
                130                135                140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
      145                150                155                160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca 528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
                165                170                175

acc cac cct gag tcc acc tga caccacacac cttatttatg cgctgagccc 579
Thr His Pro Glu Ser Thr *
                180

tactccttcc ttaatttatt tcctctcacc ctttatttat ga 621

<210> 38
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-29

<400> 38
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1      5      10      15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
      20      25
Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
      35      40      45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
      50      55      60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
      65      70      75      80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
      85      90      95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
      100                105                110

```

Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 39
 <211> 531
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> met IL-28B

<221> CDS
 <222> (1)...(531)

<400> 39
 atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15

 tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30

 ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45

 tgc aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
 Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60

 ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

 acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95

 gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

 ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

 ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag 432
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

 gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg

145		150		155		160	
ctc ctc acg cga gac	ctg aat tgt gtt gcc	agc ggg gac ctg	tgt gtc	528			
Leu Leu Thr Arg Asp	Leu Asn Cys Val Ala	Ser Gly Asp Leu	Cys Val				
	165	170	175				
tga				531			
*							

<210> 40
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> met IL-28B

<400> 40
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175